TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCCGCCCT	COGGGCIGGG	GUIGUIGUE	CIGCIGCIAC	ceciecieie	GCTACIGGIG	60
MetProProS	erGlyLeuAr	gleuleuPro	LeuLeuLeuP	roLeuLeuTr	pleneuVal	
	_	•				
CTGACGCCTG.	.00200000000000000000000000000000000000	CGCFGGACTA	TCCACCTGCA	AGACTATOGA	CATGGAGCTG	120
LeuThrProG	lyProProAl	aAlaGlyLeu	SerThrCysL	ysThrIleAs	pMetGluLeu	
				TGTCCAAGCT		180
ValLysArgL	ysArgIleGl	uAlaIleArg	GlyGlnIleL	euSerlysle	uArgLeuAla	
				COGAGGCOGT		240
SerProProS	erGinGlyGl	uValProPro	GlyProLeuP	roGluAlaVa	lleuAlaLeu	
FT 02 2 62 602	000000000000	******	A1 A1 AMAA A			202
				AACOGGAGOC		300
Tyrasnseri	urargaspar	GNSTATSGIA	GIUSETALAG	lúProGluPr	oGluProGlu	
GCCGACTACT	TANK TO THE TANK THE			m	# * # # # # * * # * # * # * # * # * # *	200
						360
vrovebiALT.	Ataronáser	nvathmarg	ASTITEMECA	alGluThrHi	EASIGIUILE	
ጥልጥር እርጎል እርጎጥ	መን አለን አለን	መእ ረን ሊማ ሊማ ሊማ ተ	naniamannan	TCTTCAACAC	አመና፣አ <i>ር</i> ፣አር <u>ዮ</u> ናቸያን	420
				hePheAsnTh		420
ratumbmat	HEDAPATIBE	+11#1#12567	***********	14-211-4-211111	1961GTUDGU	
CGAGAAGCCC	TACCICAACC	CONTRIBUTION	TYYYYYYYA	AGCTGCGTCT	ርም(ኒልርንር <u>ኔ</u>	480
				luLeuArgLe		200
			*	+	4 4 4 5 4 5 5 4 5 5 5 5 5 5 5 5 5 5 5 5	
CTCAAGTTAA	AAGTGGAGCA	GCACGTGGAG	CTGTACCAGA	AATACAGCAA	CAATTCCTGG	540
				ysfyrSerAs		•
_	_					
CGATACCTCA	GCAACCGGCT	GCTGGCACCC	AGOGACTOGO	CAGAGIGGIT	ATCTTTTGAT	600
ArgTyrLeuS	erAsnArgLe	uLeuAlaPro	SerAspSerP	roGluTrpLe	uSerPheAsp	
				·		
				AAATTGAGGG		660
ValThrGlyV	alValArgGl	nTrpLeuSer	ArgGlyGlyG	luIleGluGl	yPheArgLeu	
				AAGTGGACAT		720
SerAlaHisC	ysSerCysAs	pserargasp	AsnTirrLeuG	lnValAspIl	eAsnGlyPhe	
3.000.000000						
				TGAACCGGCC		780
TIRTIRGINA	rgargutyas	pLeuAlaunr	TTELITECIÓN	etAsnArgPr	oPheLeuLeu	
OTTO S TO COOK IN	0000000000	ar areasing	da morante da a a	****		040
					GGCAGGCGGA)	840
remiscate,	TILETOLEUGI	uargalagin	ursrex;ins	erGluPheGl	AGTAGTAGTA	
TCCCCCCTCG	COMMISSION	CCCACCCCCC	www.	<i>ር</i> የአስጥር የአስርር የ	ጠል አረትታላ/ታላምሮ	900
SerProteic	JAN SUPPLIANT	ACIONIDATE A	LUCKURATION ACIDA	lalleAsmy	TANGET PARTY.	200
	was construction of		Destructor	+~************************************	THASKITT	
CAGCTCCAAG	AAAGGACGAA	CATTOGGAAA	TOTCAGGAGC	TOCTOGAGCA	GCTGAATGGA	960
					nLeuAsnGly	

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
AAGATCAACC	TCACCTACAG	GGCGGACTTC	AACATOCCTA	TGGAGATGAC	GGAGAAGATG	1020
LysIleAsnL	euThrTyrAr	gAlaAspPhe	LysIleProM	etGluMetTh	rGluLysMet	
	ACACTGCCTT					1080
GlnLysSerT	yrThrAlaPh	eAlaIleGln	GluMetLeuG	lnAsnValPh	eLeuValPhe	
1						
	TCTCCAGCAC					1140
ArgasnasnP	heSerSerTh	rGlyTrpAsn	GluThrIleV	alValArgLe	uLeuAspGlu	
	AGACAGIGIT					1200
LeoHisGlnG	lnThrValPh	eleulysThr	ValleaGluG	luLysGlnGl	uGluArgLeu	
					********	1050
	TOTCCTCAAC					1260
ThrTrpGluM	etSerSerTh	rAlaLeuHis	LeulysserT	yrTyrTrpAr	gValGlnArg	
			******		* ** ** ***	1700
	TCATGAAGTA					1320
TyrLeuLysL	euMetLysTy	rAsnSerTyr	ATS:ITPMetV	atvatataar	aGruiterne	
3 (2/33 3 (27777777	mas mas amora	3 3 4 3 6 7 7 7 7 7 7 7	3/7333/7777999	3 3 3 3 CTYVV3 (IV)	ma o a o o	1376
	TCATCATTCG					13/0
ArgashPheL	eullelleAr	garghening	argasnenec		IAIG	
				110ga		

ifn+MMP+TGFb Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	ćc.
ATGAACAACA	GGIGGATCCT.	CCACGCTGCG	TICCICCICI	CCTTCTCCAC	CACAGCCCIC	60
MetAsnAsnA	rgTrpIleLe	uHisAlaAla	PheleuLeuC	ysPheSerTh	rimalaLeu	
					3 mc=1203 6503 65	120
TOCATCAACT	ATAAGCAGCT	CCAGCTCCAA	GAAAGGACGA	ACATICAGAA	WIGICARRA	باكد
SerIleAsnT	yrLysGlnLe	renem	GluArgThrA	EUTTEALORY	SCASGINGIO	
OMOOMOON OO	አረረረመር አመርረር	አአአርውጠማል ልሶ	CICACCTACA	GGGGGACTT	CAAGATOCCT	180
CICCIGGASC LeaferClaC	Interdence	wiwsTleAsn	LeuThrTyrA	rgAlaAspPh	eLvsIlePro	
remedarda	THEOREM	ADARAGE III.			-	
ATGGAGATGA	CGGAGAAGAT	GCAGAAGAGT	TACACTGCCT	TTGCCATCCA	AGAGATGCTC	240
MerGluMetT	hrGluLysMe	tGInLysSer	TyrThrAlaP	heAlaIleGl	nGluMetLeu	
CAGAATGICT	TICITGICIT	CAGAAACAAT	TTCTCCAGCA	CIGGGIGGAA	TGAGACTATT	300
GlnAsnValP	heLeuValPh	eyrgysnysn	PheSerSerT	hrGlyTrpAs	nGluThrIle	
			. As As As As	ለተጠናተሰውን እ ሙም ጥ	<i>አረተ</i> በአረተበአረጎ	360
GITGIACGIC	TCCTGGATGA	ACTOCACCAG	CAGACAGIGI Cladinatic ID	Later Tradb	AGTACTAGAG	200
ValValArgL	euLeuAspGl	urenHrech	. GIIIIIII VALP	rerembern	rValleuGlu	
<i>ር</i> አ አ አ አ ረም አ አ ር	አረንግአ አ አ/ጎአጣጥ	CACCITICCEAG	בביתייותיתב	ביזיניזויאריאריאריא	CTTGAAGAGC	420
Orthografia Orthografia	Includrate	᠃ᡙ᠘ᡙᡙ᠘ᠿᢊ	MetSerSerT	hrAlaLeuHi	skeukysSer	•
OTHER SOUTH	10010411910	GIIII IAG			-	
TATTACTGGA	GGGTGCAAAG	GTACCTTAAA	CTCATGAAGT	ACAACAGCIA	CGCCTGGATG	480
TyrTyrTrpA	rgValGlnAr	gTyrLeuLys	: LeuMetLysT	'yrAsnSerTy	rAlaTrpMet	
						E40
GIGGICCGAG	CAGAGATCIT	CAGGAACITI	CICATCATTC	GAAGACTIAC	CAGAAACTTC	540
ValValArgA	laGluIlePh	. eArgAsnrne	Femmeries	rgargLeum	rArgAsnPhe	
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Canacidani Canacidani	he@lu@lu@l	VELVERYPYC	LeuGlvLeuï	rpAlaGlvGl	yGlySerAla	
GTITESTEET	* INSCRINGE YOUR	. yozypozza	- 			
GCCCCACTAT	CCACCTGCAA	CACTATOGAC	ATGGAGCTGC	TGAAGCGGA	COGCATOGAG	660
AlaAlaLeuS	erThrCysLy	sThrIleAss	MetGluLeuN	/ allysArgLy	/ sArgIleGlu	
						500
GCCATCCGCG	GCCAGATCCT	GICCAAGCIC	cocciococx	7 GOCCOCCCGAR	CCAGGGGGAG	720
AlaIleArgG	lyGlnIleLe	e uSexLysLe	ı ArgleuAlas	s erproprose	e rGlnGlyGlu	
		i Concresion	ביווייצירילירווי) ב	P ልሮልልጥልማስል ካ	C COGCGACCGG	780
CANADAM FELL	Control of the contro	~ ~C1118121731 	i Tenālaīen	r vrasnser¶	rargasparg	. ••
valriurius	TALTOTERLI.	, ustunt ava.				
GIGGCCGGGG	AGAGTGCAG	A ACCOGGAGCCY	C GAGCCCTGAGC	COCACTACT	A CGCCAAGGAG	840
ValalaGlvG	luSerAlaG	l uProGluPro	o GluProGlu	A laAspTyrT	y rAlaLysGlu	
GTCACCCGCC	TECTAMICS	r ggaaaccca	C AACGAAAIC	r aigacaagr	r caagcagagr	900
ValThrArgV	alleuMetVa	a lGluThrHi	s AsmGluIle	î yrasplysi	n eLysGlnSer	
		w <i>comesses</i>	a mytanova	~ <i>_</i> ~% <i>_</i> ~%~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ስ አረም የተመጣለ አርሞች	960
ACACACAGCA	A TATATATOT	r Cricaacac	v Carcinien	CARTANATAN TAMBANATAN	r ACCTGAACCC a lProGluPro	200
'InrHisser'	TetAxMeth	n erneasinn	T DETATIONER	is thatmores	4 TTTOILULEU	

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	*****
GIGITGCICT	CCCCGGCAGA	GCIGCGICIG	CTGAGGAGGC	TCAAGITAAA	AGTGGAGCAG	1020
ValleuLeuS	erArgAlaGl	uLeuArgieu	LeuargargL	eulysleuly	sValGluGin	
CACCTOGACC	TOTACCAGAA	ATACAGCAAC	AATTCCTGGC	GATACCTCAG	CAACCGGCIG	1080
HisValGluL	euTyrGlnLy	sTyrSerAsn	AsnSerTrpA	rgTyrLeuSe	rAsnArgieu	
CIGGCACCCA	COGACTOCCC	AGAGIGGITA	TCTTTTGATG	TCACCGGAGT	TGTGCGGCAG	1140
LeuAlaProS	erAspSerPr	oGluTrpLeu	SerPheAspV	alThrGlyVa	lValArgGln	,
TGGITGAGCC	GIGGAGGGA	AATTGAGGGC	TTTOGCCTTA	GCCCCCACTG	CTCCTGTGAC	1200
TrpLeuSerA	rgGlyGlyGl	uIleGluGly	PheArgLeuS	erAlaHisCy	sSerCysAsp	
•						
AGCAGGGATA	ACACACTIGCA	AGTGGACATC	AACGGGTTCA	CTACCGGCCG	CCGAGGTGAC	1260
SerArgAspA	snThrLeuGl	nValAspIle	AsnGlyPheT	hrThrGlyAr	gArgGlyAsp	
	·	•			`	
					CCCGCTGGAG	1320
LeuAlaThrI	leHisGlyMe	tAsnArgPro	Pheleuleul	euMetAlaTh	rProL <i>e</i> uGlu	
	_					
AGGGCCCAGC	ATCTCCAAAG	CtgaTCTAGA	∞			1352
ArgAlaGlnH	isLeuGlnSe	rSerArg	•			

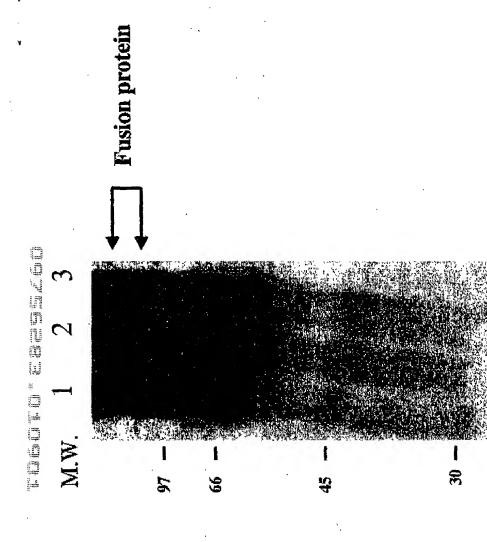
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) ZU 4 40 DU

APPSGLREEPLELPLEVELV-ETPGPPAAGESTEKTIOMEEVERKRIEAIRGOILSKERLASPPSGGE-VP-PGP
 BU TOF-8 1
 Nu TGF-8 2
              MHYCYLSAFLILH LYTVAL-----SLSTCSYLOMOGFMRKRIEATRGGTLSKLKLTSPP---EDYPEPEE
 Hu 16F-A 3
              MKHHLQRALVYLALLNFATVSL-----SLSTCTTEOFGHIKKKRYEAIRGOILSKLRLTSPP---EPTV-MTR
CE TGF-# 4
 Fg TGF-# 5
              MEY-------LINGLUGIV-LHISSIANSISTCKAYONEEVAKRRIFAIRGOTESKLKLDKTPDVDS-EK-NTY
                                           +++* +
                                                        + +++++++++ + *
                                                100
              LPEAVLALYMSIRDRYAGESAEPE-PEF------EADYYAKEYTRYLMV----ETHHETYDKFKOSTHSTYNEF
Hu fGF-# 1
HU YGF-8 Z
              VPPEVISITESTROLL -- OEKASR-RAAACERERSDEETTAKEVYKIDHPPFFPS-ERAIPPTFTRPT-FRIVEF
Hu TGF-# 3
             VPYGYLALY<u>HSI</u>RELL--EEHGER-KEEGCTGEHTESEYYAKEIHKFOMIGGLAE-HHELAVCPKGII-SKVFRF
              Ck TGF-8 4
Fà TGF-# 5
              Pseaff-ly<u>hst</u>le-virekatre-eeghvghdomiodyyakovyrf----estteledhefkfk------f
                 140
                                            160
Hu TGF-8 1
             WISEL-----RE-AVPEPVLLS-RAELHLLRUKL----KV-EOHVELYO-----KYSNWSURYLSHRULAPSDSPE
HA TGF-# 2
             DVSA------NEKNASHLA-KAEFRAERLONPK-ARAPEOR LELYO LLKSKOL TEPTORY LOSKVAKTRAEGE
Hu TGF-8 3
             <u>NYS</u>S------YEK<u>HRI</u>NLF-HAEFHALRAPHPS-SKRHEDRIELFOILRP-DEHIAKORYIGGKHLPİRGTAE
Ck YGF-B 4
             TASSSCSTSSRVRAEVGGRALLHRAELRHLROKAAADSAGTEDRLELYDGYG-----NESURTLHGRSYRATADDE
Fg TGF-B 5
             MASNY----RENYCON-SLLH-HAELRNYK-KOTO--KUNDORNELFW--KYGENGTTKSRYLESKYTTPYTOGE
                                    ** *
                  200
             WESTONTONIERGGETEGFRESAICSE ------DSRONTLONDIN-GFTTGR-----ROBERTI----
Hu TGF-# 1
             WLSFDYTDAVHEULHIKDRILGFEISLINGFETFVPSHILTI I PHKSEELEARFA-GIDGISTYTSCOOKTIKSTRK
HU TGF-8 2
HU TGF-# 3
             wlsfoyidivrewlerreshlgleisincpchtfop-kgdilehihevheikfk-gvoheddhgredigrlk---k
CR TGF-# 4
             WESFORTDANKOWLSGSELLGYFKLSVHCPCEHGPG-HADERRISIEGFEGG------REDNGSIA---K
             MINSFOYTKTYNEULKRAEENEGFGLOPAGKG ------PTPDAKD----- LOTEGFPAL-RODLASL--SSK
fg TGF-# 5
             * ***** * **
                                                  1 280
HU TGF-8 1
             ---- Highwrpflelmatplera-dh--loss---Rhrraldthycfsst--Eknccvrolyidfrkolgwkwinep
Hu TGF-# 2
             kwsgrt---Phillimelpstrl-Eso----Olnrrkkraldarycfrhy--Ophcclrply)ofkrolgjrwinep
Hu TGF-B 3
             QEONN--H-PKLILMMIPPHRL-DNPGGGQ---RKKRALDTNYCFRHL--EENCCVRPLYIDFRODLGWKWVHEP
CK TGF-8 4
             -kirr---y-pyvlahalpaerane----liisa----rrrrdlotdycfgpgtdekhccvrplyidfrkolowkwihep
Fo TGF-# 5
             ENT ....KPYL - .NITSHPAERIDIYY SS---RKKRGVGOEYCFGNN - GPNCCVKPLYINFRKOLGVKVIHEP
                                                       + * +
                  250
                                                         360
Ru TGF-# 1
             kgyhanfolgpopytwsi otoyskylal yngunpgasaapecypoaleplp 1 vyyygrkykyegl swii vrsckos
Bu TGF-# 2
             KGYXANFCAGACPYLVSSOTOHSRYLSLYHY I NPEASA SPCCVSODLEPLTIL YY I GKTPKTEOL SHHTVKSCKCS
Ru TGF-# 3
             KGYYAHFCSGPCPYLRSADT I HSTYLGLYNTL NPEASASPCCYPOOLEPLT I LYYYGRTPKYEGLSNHYYK SCKCS
Ck TGF-# 4
             EGYMANFCHGPCPY INSADTOTIEVLÄLTNOHNPGASAACCVPGTLDPLPTTYVGRNYRVEGLSHNVVRACKCS
fg 165-8 5
             KGTEANYCEGHCPY I USHQT QYSKYL SLYNQHHPGAS I SPCCYPOYL EPLP I I YYYGR I AKYEOL SHHYYR SCHCS
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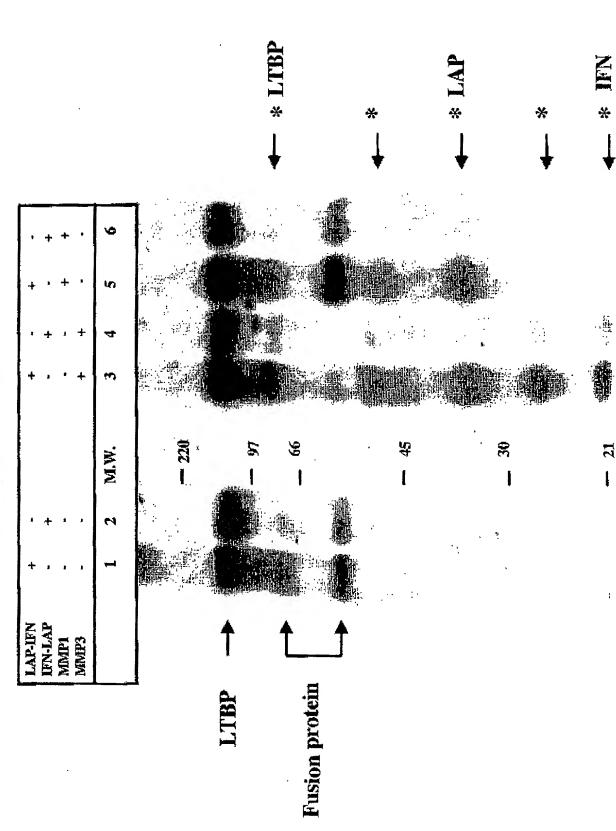
Protein	- Sequence	Reference	
MMP-I/MMP-8		DA	
Human type I collagen (al)	Ala-Pro-Gin-Gly-ns ~ Ilons-Ala-Gly-Gin	80 80	
Human type I collagen (a2)	Gly-Pro-Gin-Gly-15 - Leu-176-Leu-Gly-Ala	80 80	
Human type II collagen	Gly-Pro-Gin-Gly775 - Leuris-Ala-Gly-Gin	80 80	
Human type III collagen	Gly-Pro-Leu-Glyma-Plemo-Ala-Gly-lle	84	
Human az macroglobulin	Gly-Pro-Glu-Glysm - Leussa-Arg-Val-Gly	84	
Rat as-macroglobulin	Ata-Ala-Tyr-Hisssi-Leussr-Val-Ser-Gin	84	
Rat az macroglobulin	Met-Asp-Ala-Pheson - Leutor-Glu-Ser-Ser	84	
Rat at-macroglobulin	Glu-Pro-Gin-Alama - Lengu-Ala-Met-Ser	84	
Rat at-macroglobulin	Gin-Ala-Len-Alaess - Meless-Ser-Ala-Ile	79	
Chicken ovostatin	Pro-Ser-Tyr-Pheart - Leugra-Asn-Ala-Gly	84	
Human pregnancy zone protein	Tyr-Glu-Ala-Glyos: - Leucso-Gly-Val-Val	84	
Human pregnancy zone protein	Ala-Gly-Leu-Glyes Vales Val-Glu-Ars	84	
Human pregnancy zone protein	Ala-Gly-Leu-Gly757 - He758-Ser-Ser-Thr	85	
a - Protease inhibitor	Gly-Ala-Met-Pheisz-Leussy-Glu-Ala-lle	86	
Human aggrecan	lle-Pro-Glu-Asnus - Phesa-Phe-Gly-Val	86	
Human aggrecan	Thr-Glu-Gly-Glu373 - Alas 30-Arg-Gly-Ser	87	
Human cartilage link	Arg-Ala-He-His,6-He,7-Gln-Ala-Glu	88	
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyrpo-Leutor-Leu-Pro-Ala	54	
MMP-2	Gly-Ala-Hyp-Glyser - Leusse Glx-Gly-His	24	
Guinea pig a I (I) gelatin	Gly-Pro-Gla-Gly-go-Valini-Arg-Gly-Glu	30	
Rat al(l) gelatin	Gly-Pro-Ala-Gly277~Val278-Gly-Pro	30	
Rat al(I) gelatin	Gly-Pro-Ser-Glym - Leuzoz-Hyp-Gly-Pro	30	
Rat al (i) gelatin	Gly-Pro-Ala-Glyss: ~Gluss-Arg-Gly-Set	30	
Rat a1(1) gelatin	Gly-Ala-Lys-Gly361 ~ Leu362 Thr-Gly-Ser	30	
Rat ol (I) gelatin	Gly-Pro-Ala-Glyssa - Ginas - Asp-Gly-Pro	30	
Ret & I(I) gelatin	Gly-Pro-Ala-Gly634 - Phe635 Ala-Gly-Pro	30	
Rat #1(I) gelatin	Gly-Pro-lie-Gly ₆₇₆ ~ Asn ₆₇₇ -Val-Gly-Ala	30	
Rat orl(I) gelatin	Gly-Pro-Hyl-Gly615 ~ Ser, Arg-Gly-Ala	30	
Rat #I(i) gelatin Bovine type I collagen (# i)	Gly-Pto-Gln-Gly773~ Ile776-Ala-Gly-Gln	22	
Bovine type I collagen (a2)	Gly-Pro-Glo-Gly-ry- Leu-76-Leu-Gly-Ala	2.7	
Human aggrecan	lle-Pro-Glu-Asnas Phesez-Phe-Gly-Val	89	
Human galectin-3	Pro-Pro-Gly-Alaus ~ Tyrer-His-Gly-Ala	90	
Human cartilage link	· Are-Ala-Ile-Hisia Ile, r-Gln-Ala-Glu	, 87	
Human cartilage link	Gly-Pro-His-Leurs ~- Leurs-Val-Glu-Ala	87	
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyros - Leuron Leu-Pro-Ala	. \$8	
MMP-3	the Committee of the Co	79	
Human or macroglobulin	Gly-Pro-Glu-Glyere - Leuces-Arg-Val-Gly	79	
Human ar-macroglobulin	Arg-Val-Gly-Phene Tyrus Glu-Ser-Asp	91	
Human at antichymotrypsin	Leu-Leu-Ser-Alasso Leussi-Val-Glu-Thr	ģi.	
α ₁ -protease inhibitor	Glu-Ala-fle-Promy - Metan-Ser-lle-Pro	θi	
Antithrombin III	He-Ala-Gly-Arkins Serias-Leu-Asn-Pro	79, 92	
Chicken ovostatin	Leu-Asn-Ala-Glyers-Pheers-Thr-Ala-Ser	93	
Human aggrecau	Ile-Pro-Glu-Asnasi Phese Pho-Gly-Val	37	
Substance P	Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu	43	
Human ProMMP-1	Asp-Val-Ala-Gingo-Phen-Val-Leu-Thr	94	
Human ProMMP-3	Asp-Thr-Leu-Gluss - Valso-Met-Arg-Lys	- 94	
Human ProMMP-3	Asp-Val-Gly-Hisez-Pheen-Arg-Thr-Phe	95	
Human ProMMP-8	Asp-Ser-Gly-Glyn - Phene-Met-Leu-Thr	48	
Human ProMMP-9	Arg-Val-Ala-Giuan-Meta-Arg-Giy-Giu	48	
Human ProMMP-9	Asp-Leu-Gly-Argar - Phon-Gin-Thr-Phe Pro-Phe-Ser-Proon - Louise Val-Ala-Thr	21	
Human fibronestin	hith-hite-pet-tinett roncet_ a st. 1997- 110		

_	Sequence	Reference
Examp insulin-like growth factor	Leu-Arg-Ala-Tyr ₂₀ ~ Leu ₁₀₀ -Leu-Pro-Ala	88
binding protein-3	Ala-Pro-City-Asnim Alaire-Ser-City-Ser	88
•	Phe-Ser-Ser-Glusse~Serity-Lys-Arg-Glu	88
Bovine a I(II) collagen. N-telopeptide	Ala-Gly-Gly-Alans~Ginne-Met-Gly-Val	96
dovine al (II) collagen. N-telopeptide	Gin-Met-Gly-Value - Metim-Gin-Gly-Pro	96
Bovine a1(1X) collagen, NC2	Met-Ala-Ala-Ser - Leu-Lvs-Arg-Pro	96
Bovine a2(1X) collagen, NC2	~ Ala-Lys-Arg-Glu	96
Bovine a3(IX) collagen, NC2	~Leu-Arg-Lys-Pro	96
Bovine α I(XI) collagen, N- telopeptide	Gln-Ala-Gln-Ala-Re-Leu-Gln-Gln	96
Human cartilage link	Arg-Ala-Ile-His,, ~Ile, -Gln-Ala-Glu	87
Bovine insulin. B chain	Leu-Val-Glu-Alais Leuis-Tyr-Leu-Val	97
Bovine insulin. B chain	Glu-Ala-Leu-Tyris - Leuiz-Val-Cys-Gly	21, 97
MMP-7	- · · · · · · · · · · · · · · · · · · ·	-
Human aggrecan	He-Pro-Glu-Asnat ~ Phenay-Phe-Gly-Val	89
Human carrilage link	Gly-Pro-His-Leum-Leum-Val-Glu-Ala	87
Human prourokinase	Pro-Pro-Glu-Glung-Leum-Lys-Phe-Gin	98
ММР-9		
Human type V collagen (a1)	Gly-Pro-Pro-Gly+39 ~ Val+40-Val-Gly-Pro	99
Human type V collagen (a2)	Gly-Pro-Pro-Gly+15~ LeuHe-Arg-Gly-Glu	99
Human type XI collagen (a1)	Gly-Pro-Gly-Glyan ~ Valeso-Val-Gly-Pro	99
Human aggrecan	lie-Pro-Glu-Asn ₁₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Alasz ~ Tyres-His-Gly-Ala	90
Human cartilage link	Arg-Ala-lia-Histo lietz-Gin-Ala-Glu	87
MMP-10		
Human cartilage link	Arg-Ale-ile-Hisis ~ Ile, ~ Gln-Ala-Glu	87
Human carrilage link	Gly-Pro-His-Leuzz-Leuzz-Val-Glu-Ala	87

F1g. 5

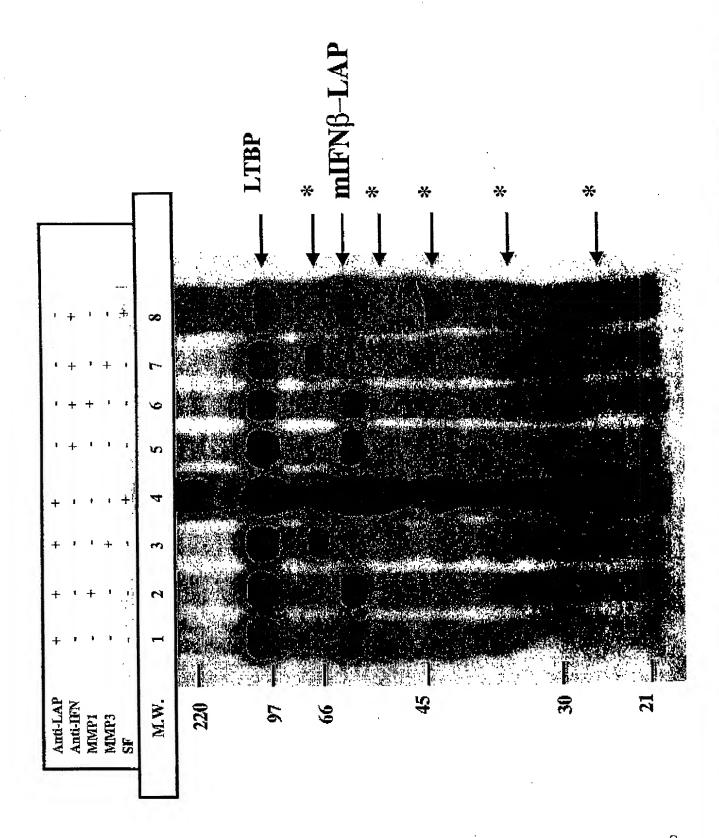


F18.

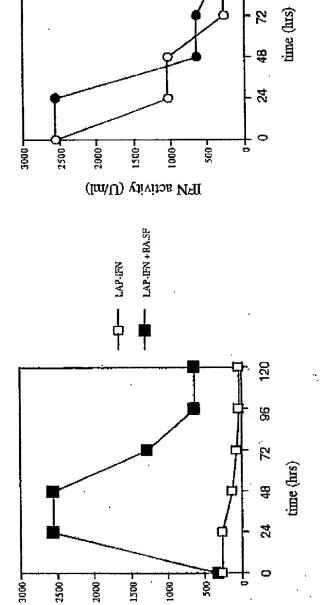


F1g.

Fig. Ba





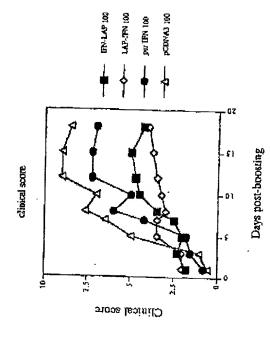


IFN activity (Units/ml)

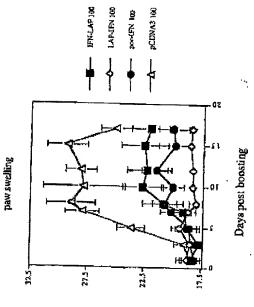
96

Fig.





£19, 10



paw swelling (mmx10-1)